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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/510,716	10/18/2004	Yoshihiro Hakamada	260068US0PCT	2844

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OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
1940 DUKE STREET
ALEXANDRIA, VA 22314

EXAMINER	
RAGHU, GANAPATHIRAM	
ART UNIT	**PAPER NUMBER**
1652	

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
3 MONTHS	01/18/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

Office Action Summary	Application No.	Applicant(s)	
	10/510,716	HAKAMADA ET AL.	
	Examiner	Art Unit	
	Ganapathirama Raghu	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *26 September 2006*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-8 and 10-22* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-8 and 10-22* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

Application Status

In response to the Office Action (FOAM) mailed on June 30, 2006, applicants' Sep. 05, 2006 response and amendments are acknowledged. Said amendment, amended claims 1-5, 8, canceled claim 9 and added new claims 10-22. Thus, claims 1-8 and 10-22 are pending in the instant Office Action and are now under consideration.

Objections and rejections not reiterated from previous action are hereby withdrawn.

Claim Objections

Claim 1and 8 are objected to because of the following informalities: claim 1 and 8 recite the phrase "...% homology", the metes and bounds of this phrase is not clear and examiner suggests amending the claims to recite "...% sequence homology".

Claims 6-7 and claims 19-20 and claims 8 and 20 depending therefrom are objected to because of the following informalities: Claims 6-7 and claims 19-20 recite the phrase "gene". It is not clear to the examiner as to what this phrase means in the context of the above claims. A "gene" could comprise other upstream and downstream elements such as regulatory sequences/elements, enhancers, promoters and un-translated regions (UTRs). Therefore, examiner suggests amending the claims to recite "an isolated polynucleotide". Appropriate correction is required.

Maintained- Claim Rejections: 35 USC § 112-First Paragraph

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to

which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Written Description

Claim 1 and claims 6-8, 10-11, 14, 19-22 depending therefrom are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claim 1 is directed to a mutated alkaline cellulase obtained by deleting, from a cellulase having the amino acid sequence represented by SEQ ID NO: 2 or a homologous amino acid sequence exhibiting at least 95% homology to SEQ ID NO: 2, a peptide consisting of one or more amino acid residues chosen from positions 343-377 of SEQ ID NO: 2 or from corresponding positions of said homologous amino acid sequence and replacing the peptide with an insertion peptide having 2-15 amino acids into at least one deleted position and having alkaline cellulase activity. Claims 6-9 and 19-22 are directed to a gene encoding said mutated polypeptide, vector and an isolated host cell. Claims 10-11 are directed to method of producing said polypeptides and claim 14 is directed to a mutated alkaline comprising the sequence of SEQ ID NO: 7 or 8 or 9, a peptide consisting of one or more amino acid residues chosen from the positions corresponding to the 343-377 the positions of SEQ ID NO: 2 and replacing the peptide with an insertion peptide having 2-15 amino acid residues.

Claims 1, 6-8, 10-11, 14 and 19-22 are rejected under this section 35 U.S.C. 112, because the claims are directed to a genus of polypeptides, i.e., mutated alkaline cellulase

obtained by deleting from a cellulase having the amino acid sequence represented by SEQ ID NO: 2 or a homologous amino acid sequence an amino acid sequence exhibiting at least 95% homology to SEQ ID NO: 2, a peptide consisting of one or more amino acid residues chosen from positions 343-377 of SEQ ID NO: 2 or from corresponding positions of said homologous amino acid sequence and replacing the peptide with an insertion peptide having 2-15 amino acids into at least one deleted position and having alkaline cellulase activity or a enzyme homologous thereto, with no support in the specification for the structural details of all the species encompassed in the genus associated with the function i.e., alkaline cellulase activity, vector and host cell has been provided in the specification for the claims. The specification discloses the isolation of a polypeptide from *Bacillus sp.*, KSM-S237, a cellulase with SEQ ID NO: 2 (Egl-237) and three mutants with alkaline cellulase activity by deleting the amino acid residues spanning the region of 357-362 of SEQ ID NO: 2 and inserting alanine-glycine-alanine or alanine-histidine-alanine or alanine-arginine-alanine (Example 1, page 13 of Specification SEQ ID NOs; 7-9), the disclosed species which replaces a short peptide region with three specific other short peptides i.e., alanine-glycine-alanine or alanine-histidine-alanine or alanine-arginine-alanine would not be representative of scope of modification encompassed in claim 1, such that claim 1 includes alkaline cellulases obtained by deleting, from a cellulase having the amino acid sequence represented by SEQ ID NO: 2 or a homologous amino acid sequence an amino acid sequence exhibiting at least 95% homology to SEQ ID NO: 2, a peptide consisting of one or more amino acid residues chosen from positions 343-377 of SEQ ID NO: 2 or from corresponding positions of said homologous amino acid sequence and replacing the peptide with an

insertion peptide having 2-15 amino acids into at least one deleted position and having alkaline cellulase activity. No information, beyond the characterization of the polypeptide, a cellulase with SEQ ID NO: 2 (Egl-237) and three mutants (SEQ ID NOs: 7-9) with alkaline cellulase activity by deleting the amino acid residues spanning the region of 357-362 of SEQ ID NO: 2 has been provided by the applicants, which would indicate that they had possession of claimed a mutated alkaline cellulase obtained by deleting from a cellulase having the amino acid sequence represented by SEQ ID NO: 2 or a homologous amino acid sequence exhibiting at least 95% homology to SEQ ID NO: 2, a peptide consisting of one or more amino acid residues chosen from positions 343-377 of SEQ ID NO: 2 or from corresponding positions of said homologous amino acid sequence and replacing the peptide with an insertion peptide having 2-15 amino acids into at least one deleted position and having alkaline cellulase activity. The specification does not contain any disclosure of the sequence and structure of all the polypeptides within the scope of the claimed genus. The disclosed information is insufficient to put one of skill in the art in possession of the attributes and features of all species within the claimed genus of polypeptides. Therefore, one skilled in the art cannot reasonably conclude that applicant had possession of the claimed invention at the time the instant application was filed. Applicant is referred to the revised guidelines concerning compliance with the written description requirement of U.S.C. 112, first paragraph, published in the Official Gazette and also available at www.uspto.gov.

Applicants' have traversed the rejection by pointing out that claims have been duly amended to recite that the defined sequences to be at least 95% homology to SEQ

ID NO: 2 and have referred to written description guidelines of MPEP and to a reversal of BPAI case (*Ex parte Bandman*) in support of their arguments.

Applicants' arguments have been considered and found to be non-persuasive as disclosed species is not representative of the structure of all the species encompassed in the genus and specification does not contain any disclosure of the sequence and structure of all the polypeptides within the scope of the claimed genus for the reasons cited below. Furthermore, examiner would like to point that the cited court rulings cannot be applied or construed as a "blanket ruling" for all cases, as the fact pattern of each and every case is different. This becomes obvious in the light of inventors' admission on record in pages 8-9 of specification, wherein it is stated "Three-dimensional structural analysis through homology modeling (Ozawa et al., Protein Eng., 14, 501-504, 2001) suggests that the amino acid region at the 343rd to 377th positions of SEQ ID NO: 2 (should be read as SEQ ID NO: 2, due to the amendment from SEQ ID NO: 1 to 2) is located relatively distant from the active site of Egl-237 and therefore a high degree of freedom, and is suggested to be region that forms the loop structure that is intimately involved in **maintaining the cellulase structure**".

It is well known in the art that structure correlates with function and furthermore any amino acid residue or any number of amino acid residue substitutions may not be tolerated, as such substitutions may not yield a structure correlated with the desired functional activity of the molecule.

The disclosed information is insufficient to put one of skill in the art in possession of the attributes and features of all species within the claimed genus of polypeptides. Clearly the recited genera include many proteins with very different structures with no

support in the specification with the correlated functional activity of the molecule as claimed.

Enablement

Claim 1 and claims 6-8, 10-11, 14, 19-22 depending therefrom are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a polypeptide from *Bacillus sp.*, KSM-S237, a cellulase with SEQ ID NO: 2 (Egl-237) and three mutants with alkaline cellulase activity by deleting the amino acid residues spanning the region of 357-362 of SEQ ID NO: 2, and inserting alanine-glycine-alanine or alanine-histidine-alanine or alanine-arginine-alanine, expression vector and isolated host cell, does not reasonably provide enablement for any isolated mutated alkaline cellulase from any source obtained by deleting from a cellulase having the amino acid sequence represented by SEQ ID NO: 2 or a homologous amino acid sequence an amino acid sequence exhibiting at least 95% homology to SEQ ID NO: 2, a peptide consisting of one or more amino acid residues chosen from positions 343-377 of SEQ ID NO: 2 or from corresponding positions of said homologous amino acid sequence and replacing the peptide with an insertion peptide having 2-15 amino acids into at least one deleted position and having alkaline cellulase activity or a enzyme homologous thereto, to a gene encoding said mutated polypeptide, vector and an isolated host cell and claim 14 directed to a mutated alkaline comprising the sequence of SEQ ID NO: 7 or 8 or 9 a peptide consisting of one or more amino acid residues chosen from the positions corresponding to the 343rd-377th positions of SEQ ID NO: 2 and replacing the peptide with an insertion peptide having 2-15 amino acid residues. The specification does not enable any person

skilled in the art to which it pertains, or with which it is most nearly connected, to make and or use the invention commensurate in scope with the claims.

Factors to be considered in determining whether undue experimentation is required are summarized in *In re Wands* (858 F.2d 731, 8 USPQ 2nd 1400 (Fed. Cir. 1988)) as follows: (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claim(s).

Claims 1, 6-8, 10-11, 14 and 19-22 are so broad as to encompass any mutated alkaline cellulase from any source obtained by deleting from a cellulase having the amino acid sequence represented by SEQ ID NO: 2 or a homologous amino acid sequence an amino acid sequence exhibiting at least 95% homology to SEQ ID NO: 2, a peptide consisting of one or more amino acid residues chosen from positions 343-377 of SEQ ID NO: 2 or from corresponding positions of said homologous amino acid sequence and replacing the peptide with an insertion peptide having 2-15 amino acids into at least one deleted position and having alkaline cellulase activity or a enzyme homologous thereto, to a gene encoding said mutated polypeptide, vector and an isolated host cell and claim 14 directed to a mutated alkaline comprising the sequence of SEQ ID NO: 7 or 8 or 9 a peptide consisting of one or more amino acid residues chosen from the positions corresponding to the 343rd-377th positions of SEQ ID NO: 2 and replacing the peptide with an insertion peptide having 2-15 amino acid residues. The scope of the claims are not commensurate with the enablement provided by the disclosure with regard to the extremely large number of polypeptides broadly encompassed by the claims. Since the

amino acid sequence of a protein encoded by a polynucleotide determines its structural and functional properties, predictability of which changes can be tolerated in a protein's amino acid sequence and obtain the desired activity requires knowledge and guidance with regard to which amino acids in the protein's sequence and the respective codons in its polynucleotide, if any, are tolerant of modification and which are conserved (i.e. expectedly intolerant to modification), and detailed knowledge of the ways in which the encoded proteins' structure relates to its function. However, in this case the disclosure is limited to an isolated polypeptide from *Bacillus sp.*, KSM-S237, a cellulase with SEQ ID NO: 2 (Egl-237) and three mutants with alkaline cellulase activity by deleting the amino acid residues spanning the region of 357-362 of SEQ ID NO: 2, and inserting alanine-glycine-alanine or alanine-histidine-alanine or alanine-arginine-alanine, does not reasonably provide enablement for any isolated mutated alkaline cellulase from any source obtained by deleting, from a cellulase having the amino acid sequence represented by SEQ ID NO: 2 or a homologous amino acid sequence exhibiting at least 95% homology to SEQ ID NO: 2, a peptide consisting of one or more amino acid residues chosen from positions 343-377 of SEQ ID NO: 2 or from corresponding positions of said homologous amino acid sequence and replacing the peptide with an insertion peptide having 2-15 amino acids into at least one deleted position and having alkaline cellulase activity or a enzyme homologous thereto, to a gene encoding said mutated polypeptide, vector and an isolated host cell and claim 14 directed to a mutated alkaline comprising the sequence of SEQ ID NO: 7 or 8 or 9 a peptide consisting of one or more amino acid residues chosen from the positions corresponding to the 343rd-377th positions of SEQ ID NO: 2 and replacing the peptide with an insertion peptide having 2-15 amino acid

residues. It would require undue experimentation of the skilled artisan to make and use the claimed polypeptides and encoding polynucleotides. The specification is limited to teaching the use of a cellulase, an isolated polypeptide from *Bacillus sp.*, KSM-S237, a cellulase with SEQ ID NO: 2 (Egl-237) and three mutants with alkaline cellulase activity by deleting the amino acid residues spanning the region of 357-362 of SEQ ID NO: 2, and inserting alanine-glycine-alanine or alanine-histidine-alanine or alanine-arginine-alanine, but provides no guidance with regard to the making of other variants and mutants from any source or with regard to other uses. In view of the great breadth of the claims, amount of experimentation required to make the claimed polypeptides, the lack of guidance, working examples, and unpredictability of the art in predicting function from a polypeptide primary structure (e.g., see Ngo et al. in The Protein Folding Problem and Tertiary Structure Prediction, 1994, Merz et al. (ed.), Birkhauser, Boston, MA, pp. 433 and 492-495), the claimed invention would require undue experimentation. As such, the specification fails to teach one of ordinary skill how to use the full scope of the polypeptides encompassed by these claims.

While enzyme isolation techniques, recombinant and mutagenesis techniques are known, and it is not routine in the art to screen for multiple substitutions or multiple modifications as encompassed by the instant claims, the specific amino acid positions within a protein's sequence where amino acid modifications can be made with a reasonable expectation of success in obtaining the desired activity/utility are limited in any protein and the result of such modifications is unpredictable. In addition, one skilled in the art would expect any tolerance to modification for a given protein to diminish with each further and additional modification, e.g. multiple substitutions or deletions.

The specification does not support the broad scope of the claims which encompass all modifications of an isolated polypeptide encoding an alkaline cellulase from any source, obtained by deleting from a cellulase having the amino acid sequence represented by SEQ ID NO: 2 or a homologous amino acid sequence exhibiting at least 95% homology to SEQ ID NO: 2, a peptide consisting of one or more amino acid residues chosen from positions 343-377 of SEQ ID NO: 2 or from corresponding positions of said homologous amino acid sequence and replacing the peptide with an insertion peptide having 2-15 amino acids into at least one deleted position and having alkaline cellulase activity or a enzyme homologous thereto, to a gene encoding said mutated polypeptide, vector and an isolated host cell and claim 14 directed to a mutated alkaline comprising the sequence of SEQ ID NO: 7 or 8 or 9 a peptide consisting of one or more amino acid residues chosen from the positions corresponding to the 343rd-377th positions of SEQ ID NO: 2 and replacing the peptide with an insertion peptide having 2-15 amino acid residues, because the specification does not establish: (A) regions of an alkaline cellulase having replacements of all or a portion of a 35 residue long fragment (from positions 343rd to 377th position) with 2-15 unspecified amino acids in the protein/polynucleotide structure without affecting the activity of the encoded cellulase; (B) the general tolerance of the polypeptide and the polynucleotide encoding cellulase to said modification and extent of such tolerance; (C) a rational and predictable scheme for said modification with any amino acid residue or the respective codon in the polynucleotide with an expectation of obtaining the desired biological function; and (D) the specification provides insufficient guidance as to which of the essentially infinite possible choices is likely to be successful.

Thus, applicants have not provided sufficient guidance to enable one of ordinary skill in the art to make and use the claimed invention in a manner reasonably correlated with the scope of the claims broadly including polypeptides with an enormous number of modifications. The scope of the claims must bear a reasonable correlation with the scope of enablement (*In re Fisher*, 166 USPQ 19 24 (CCPA 1970)). Without sufficient guidance, determination of polypeptides having the desired biological characteristics is unpredictable and the experimentation left to those skilled in the art is unnecessarily, and improperly, extensive and undue. See *In re Wands* 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988).

Applicants' have traversed both the written description and enablement rejections with the same arguments and point out that claims have been duly amended to recite that the defined sequences to be at least 95% homology to SEQ ID NO: 2 and have referred to written description guidelines of MPEP and to a reversal of BPAI case (*Ex parte Bandman*) in support of their written description and enablement traversal arguments.

Applicants' arguments have been considered and found to be non-persuasive for the same reasons in countering the applicants' arguments for written description. Although applicants have shown how to make the variants by way of three examples (SEQ ID NOs: 7-9), applicants have not established how to use other claimed variants as encompassed by the claims, i.e., the structure-function correlation is not established in the specification for all the variants and mutants. While methods to produce variants of a known sequence, such as insertion mutagenesis, site-specific mutagenesis, random mutagenesis, etc., are well known to the skilled artisan, producing variants useful as

claimed; any mutated alkaline cellulase from any source obtained by deleting from a cellulase having the amino acid sequence represented by SEQ ID NO: 2 or a homologous amino acid sequence an amino acid sequence exhibiting at least 95% homology to SEQ ID NO: 2, a peptide consisting of one or more amino acid residues chosen from positions 343-377 of SEQ ID NO: 2 or from corresponding positions of said homologous amino acid sequence and replacing the peptide with an insertion peptide having 2-15 amino acids into at least one deleted position and having alkaline cellulase activity or a enzyme homologous thereto, to a gene encoding said mutated polypeptide, vector and an isolated host cell and claim 14 directed to a mutated alkaline comprising the sequence of SEQ ID NO: 7 or 8 or 9 a peptide consisting of one or more amino acid residues chosen from the positions corresponding to the 343rd-377th positions of SEQ ID NO: 2 and replacing the peptide with an insertion peptide having 2-15 amino acid residues, requires that one of ordinary skill in the art know or be provided with guidance for the selection of which of the infinite number of variants have the activity. Without such guidance, one of ordinary skill would be reduced to the necessity of producing and testing all of the virtually infinite possibilities. For the rejected claims, this would clearly constitute **undue** experimentation.

Summary of Pending Issues

The following is a summary of issues pending in the instant application.

1) Claims 1, 6-8, 10-11, 14 and 19-22 are rejected under 35 U.S.C. first paragraph for written description and enablement.

2) Claims 2-5, 12-13 and 15-18, are objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

Allowable Subject Matter/Conclusion

None of the claims are allowable. Claims 1-8 and 10-22 are rejected for the reasons identified in the Rejections and Summary sections of this Office Action. Applicants must respond to the objections/rejections in each of the sections in this Office Action to be fully responsive for prosecution.

THIS ACTION IS MADE FINAL. Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a). A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Final Comments

To insure that each document is properly filed in the electronic file wrapper, it is requested that each of amendments to the specification, amendments to the claims, Applicants' remarks, requests for extension of time, and any other distinct papers be submitted on separate pages.

It is also requested that Applicants identify support, within the original application, for any amendments to the claims and specification.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ganapathirama Raghu whose telephone number is 571-272-4533. The examiner can normally be reached on 8 am - 4:30 pm. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapu Achutamurthy can be reached on 571-272-0928. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300 for regular communications and for After Final communications. Any inquiry of a general nature or relating to the status of the application or proceeding should be directed to the receptionist whose telephone number is 571-272-1600.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Ganapathirama Raghu, Ph.D.
Patent Examiner
Art Unit 1652

Dec. 21, 2006.

REBECCA E. PROUTY
PRIMARY EXAMINER
GROUP ~~1800~~ 1600